



# SEQUENCE LISTING

<110> University of Maryland, Baltimore  
GALEN, James E.

<120> USE OF CLYA HEMOLYSIN FOR EXCRETION OF PROTEINS

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<140> 09/993,292

<141> 2001-11-23

<150> US 60/252,516

<151> 2000-11-22

<160> 28

<170> PatentIn version 3.3

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 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp  
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505

510

Tyr Ser Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu  
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His Phe Ala Val Pro Gln Ala Lys Gly Asn Asn Val Val Ile Thr Ser  
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Tyr Met Thr Asn Arg Gly Phe Tyr Ala Asp Lys Gln Ser Thr Phe Ala  
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Pro Ser Phe Leu Leu Asn Ile Lys Gly Lys Lys Thr Ser Val Val Lys  
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730

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cctggaagac ctttgatgaa accataaaag agttaagccg ttttaaacag gagtactcgc 240
aggaagcttc tgttttagtt ggtgatatta aagttttgct tatggacagc caggacaagt 300
attttgaagc gacacaaact gtttatgaat ggtgtggtgt cgtgacgcaa ttactctcag 360
cgtatatattt actatttgat gaatataatg agaaaaaagc atcagcccag aaagacattc 420
tcattaggat attagatgat ggtgtcaaga aactgaatga agcgcaaaaa tctctcctga 480
caagttcaca aagtttcaac aacgcttcgc gaaaactgct ggcattagat agccagttaa 540
ctaagtattt ttcggaaaaa agtagttatt tccagtcaca ggtggataga attcgtaagg 600
aagcttatgc cgggtgctgca gccggcatag tcgccgggtcc gtttggatta attatttctt 660
attctattgc tgcgggctg attgaaggga aattgattcc agaattgaat aacaggctaa 720
aaacagtgca aaatttcttt actagcttat cagctacagt gaaacaagcg aataaagata 780
tcgatgcggc aaaattgaaa ttagccactg aaatagcagc aattggggag ataaaaacgg 840
aaaccgaaac aaccagattc tacgttgatt atgatgattt aatgctttct ttattaaaag 900
gagctgcaaa gaaaatgatt aacacctgta atgaatacca acaaagacac ggtaagaaga 960
cgcttttcga ggttcctgac gtctgataca ttttcattcg atctgtgtac ttttaacgcc 1020
cgatagcgta aagaaaatga gagacggaga aaaagcgata ttcaacagcc cgataaacia 1080
gagtcgttac cgggctgacg ag 1102

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<210> 23
<211> 1102
<212> DNA
<213> Salmonella paratyphi

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<220>
<221> CDS
<222> (75)..(986)

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<400> 23
ggaggcaata ggtaggaata agttataaaa caatagctta attgcaattt atatatttaa 60

agaggcaaat gatt atg act gga ata ttt gca gaa caa act gta gag gta 110
          Met Thr Gly Ile Phe Ala Glu Gln Thr Val Glu Val
          1             5             10

gtt aaa agc gcg atc gaa acc gca gat ggg gca tta gat ttt tat aac 158
Val Lys Ser Ala Ile Glu Thr Ala Asp Gly Ala Leu Asp Phe Tyr Asn
          15             20             25

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aaa tac ctc gac cag gtt atc ccc tgg aag acc ttt gat gaa acc ata Lys Tyr Leu Asp Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile 30 35 40	206
aaa gag tta agc cgt ttt aaa cag gag tac tcg cag gaa gct tct gtt Lys Glu Leu Ser Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val 45 50 55 60	254
tta gtt ggt gat att aaa gtt ttg ctt atg gac agc cag gat aag tat Leu Val Gly Asp Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr 65 70 75	302
ttt gaa gcg aca caa act gtt tat gaa tgg tgt ggt gtc gtg acg caa Phe Glu Ala Thr Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln 80 85 90	350
tta ctc tca gcg tat att tta cta ttt gat gaa tat aat gag aaa aaa Leu Leu Ser Ala Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys 95 100 105	398
gca tca gcg cag aaa gac att ctc atc agg ata tta gat gat ggc gtc Ala Ser Ala Gln Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val 110 115 120	446
aat aaa ctg aat gaa gcg caa aaa tct ctc ctg gga agt tca caa agt Asn Lys Leu Asn Glu Ala Gln Lys Ser Leu Leu Gly Ser Ser Gln Ser 125 130 135 140	494
ttc aac aac gct tca gga aaa ctg ctg gca tta gat agc cag tta act Phe Asn Asn Ala Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr 145 150 155	542
aat gat ttc tcg gaa aaa agt agt tat ttc cag tca cag gtg gat aga Asn Asp Phe Ser Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg 160 165 170	590
att cgt aag gaa gct tat gcc ggt gct gca gca ggc ata gtc gcc ggt Ile Arg Lys Glu Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly 175 180 185	638
ccg ttt gga tta att att tcc tat tct att gct gcg ggc gtg att gaa Pro Phe Gly Leu Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu 190 195 200	686
ggg aaa ttg att cca gaa ttg aat gac agg cta aaa gca gtg caa aat Gly Lys Leu Ile Pro Glu Leu Asn Asp Arg Leu Lys Ala Val Gln Asn 205 210 215 220	734
ttc ttt act agc tta tca gtc aca gtg aaa caa gcg aat aaa gat atc Phe Phe Thr Ser Leu Ser Val Thr Val Lys Gln Ala Asn Lys Asp Ile 225 230 235	782
gat gcg gca aaa ttg aaa tta gcc act gaa ata gca gca att ggg gag Asp Ala Ala Lys Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu 240 245 250	830

ata aaa acg gaa acc gaa aca acc aga ttc tac gtt gat tat gat gat	878
Ile Lys Thr Glu Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp	
255 260 265	

tta atg ctt tct tta cta aaa gga gct gca aag aaa atg att aac acc	926
Leu Met Leu Ser Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr	
270 275 280	

tgt aat gaa tac caa caa agg cac ggt aag aag acg ctt ctc gag gtt	974
Cys Asn Glu Tyr Gln Gln Arg His Gly Lys Lys Thr Leu Leu Glu Val	
285 290 295 300	

cct gac atc tga tacattttca ttcgctctgt ttacttttaa cgcccgatag	1026
Pro Asp Ile	

cgatgaagaaa atgagagacg gagaaaaagc gatattcaac agcccgataa acaagagtcg	1086
ttaccgggct ggcgag	1102

<210> 24  
 <211> 303  
 <212> PRT  
 <213> Salmonella paratyphi

<400> 24

Met Thr Gly Ile Phe Ala Glu Gln Thr Val Glu Val Val Lys Ser Ala
1 5 10 15

Ile Glu Thr Ala Asp Gly Ala Leu Asp Phe Tyr Asn Lys Tyr Leu Asp
20 25 30

Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
35 40 45

Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
50 55 60

Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65 70 75 80

Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
85 90 95

Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
100 105 110

Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Asn Lys Leu Asn  
115 120 125

Glu Ala Gln Lys Ser Leu Leu Gly Ser Ser Gln Ser Phe Asn Asn Ala  
130 135 140

Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser  
145 150 155 160

Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu  
165 170 175

Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu  
180 185 190

Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile  
195 200 205

Pro Glu Leu Asn Asp Arg Leu Lys Ala Val Gln Asn Phe Phe Thr Ser  
210 215 220

Leu Ser Val Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys  
225 230 235 240

Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu  
245 250 255

Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser  
260 265 270

Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr  
275 280 285

Gln Gln Arg His Gly Lys Lys Thr Leu Leu Glu Val Pro Asp Ile  
290 295 300

<210> 25  
<211> 904  
<212> DNA  
<213> Shigella flexneri

<220>  
<221> CDS

<222> (1)..(342)

<400> 25

atg act gaa atc gtt gca gat aaa acg gta gaa gta gtt aaa aac gca	48
Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala	
1 5 10 15	

atc gaa acc gca gat gga gca tta gat ctt tat aat aaa tat ctc gat	96
Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp	
20 25 30	

cag gtc atc ccc tgg cag acc ttt gat gaa acc ata aaa gag tta agt	144
Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser	
35 40 45	

cgc ttt aaa cag gag tat tca cag gca gcc tcc gtt tta gtc ggc gat	192
Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp	
50 55 60	

att aaa acc tta ctt atg gat agc cag gat aag tat ttt gaa gca acc	240
Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr	
65 70 75 80	

caa aca gtg tat gaa tgg tgt ggt gtt gcg acg caa ttg ctc gca gcg	288
Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala	
85 90 95	

tat att ttg cta ttt gat gag tac aat gag aag aaa gca tcc gcc cct	336
Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Pro	
100 105 110	

cat taa ggtactggat gacggcatca cgaagctgaa tgaagcgcaa aattccctgc	392
His	

tggttaagctc acaaagtttc aacaacgctt ccgggaaact gctggcggtta gatagccagt	452
---------------------------------------------------------------------	-----

taaccaatga tttttcagaa aaaagcagct atttccagtc acaggtagat aaaatcagga	512
-------------------------------------------------------------------	-----

aggaagcgta tgccggtgcc gcagccggtg tcgtcgccgg tccatttggt ttaatcattt	572
-------------------------------------------------------------------	-----

cctatttctat tgctgcgggc gtagttgaag ggaaactgat tccagaattg aagaacaagt	632
--------------------------------------------------------------------	-----

taaaatctgt gcagagtttc tttaccaccc tgtctaacac ggttaaacia gcgaataaag	692
-------------------------------------------------------------------	-----

atatcgatgc cgccaaattg aaattaacca ccgaaatagc cgccatcggg gagataaaaa	752
-------------------------------------------------------------------	-----

cggaaactga aaccaccaga ttctatgttg attatgatga tttaatgctt tctttgctaa	812
-------------------------------------------------------------------	-----

aagcagcggc caaaaaaatg attaacacct gtaatgagta tcagaaaaga cacggtaaaa	872
-------------------------------------------------------------------	-----

agacactctt tgaggtacct gaagtctgat aa	904
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<210> 26

<211> 113

<212> PRT  
 <213> Shigella flexneri

<400> 26

Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala  
 1 5 10 15

Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp  
 20 25 30

Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser  
 35 40 45

Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp  
 50 55 60

Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr  
 65 70 75 80

Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala  
 85 90 95

Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Pro  
 100 105 110

His

<210> 27  
 <211> 1080  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (121)..(1032)

<400> 27  
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 attaatagtt gtaaaacagg agtttcatta caatttatat atttaaagag gcgaatgatt 120  
 atg act gaa atc gtt gca gat aaa acg gta gaa gta gtt aaa aac gca 168  
 Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala  
 1 5 10 15

atc gaa acc gca gat gga gca tta gat ctt tat aat aaa tat ctc gat Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp 20 25 30	216
cag gtc atc ccc tgg cag acc ttt gat gaa acc ata aaa gag tta agt Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser 35 40 45	264
cgc ttt aaa cag gag tat tca cag gca gcc tcc gtt tta gtc ggc gat Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp 50 55 60	312
att aaa acc tta ctt atg gat agc cag gat aag tat ttt gaa gca acc Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr 65 70 75 80	360
caa aca gtg tat gaa tgg tgt ggt gtt gcg acg caa ttg ctc gca gcg Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala 85 90 95	408
tat att ttg cta ttt gat gag tac aat gag aag aaa gca tcc gcc cag Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln 100 105 110	456
aaa gac att ctc att aag gta ctg gat gac ggc atc acg aag ctg aat Lys Asp Ile Leu Ile Lys Val Leu Asp Asp Gly Ile Thr Lys Leu Asn 115 120 125	504
gaa gcg caa aaa tcc ctg ctg gta agc tca caa agt ttc aac aac gct Glu Ala Gln Lys Ser Leu Leu Val Ser Ser Gln Ser Phe Asn Asn Ala 130 135 140	552
tcc ggg aaa ctg ctg gcg tta gat agc cag tta acc aat gat ttt tca Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser 145 150 155 160	600
gaa aaa agc agc tat ttc cag tca cag gta gat aaa atc agg aag gaa Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Lys Ile Arg Lys Glu 165 170 175	648
gca tat gcc ggt gcc gca gcc ggt gtc gtc gcc ggt cca ttt gga tta Ala Tyr Ala Gly Ala Ala Ala Gly Val Val Ala Gly Pro Phe Gly Leu 180 185 190	696
atc att tcc tat tct att gct gcg ggc gta gtt gaa gga aaa ctg att Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Val Glu Gly Lys Leu Ile 195 200 205	744
cca gaa ttg aag aac aag tta aaa tct gtg cag aat ttc ttt acc acc Pro Glu Leu Lys Asn Lys Leu Lys Ser Val Gln Asn Phe Phe Thr Thr 210 215 220	792
ctg tct aac acg gtt aaa caa gcg aat aaa gat atc gat gcc gcc aaa Leu Ser Asn Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys 225 230 235 240	840

ttg	aaa	tta	acc	acc	gaa	ata	gcc	gcc	atc	ggt	gag	ata	aaa	acg	gaa	888
Leu	Lys	Leu	Thr	Thr	Glu	Ile	Ala	Ala	Ile	Gly	Glu	Ile	Lys	Thr	Glu	
				245					250						255	

act	gaa	aca	acc	aga	ttc	tac	gtt	gat	tat	gat	gat	tta	atg	ctt	tct	936
Thr	Glu	Thr	Thr	Arg	Phe	Tyr	Val	Asp	Tyr	Asp	Asp	Leu	Met	Leu	Ser	
			260					265					270			

ttg	cta	aaa	gaa	gcg	gcc	aaa	aaa	atg	att	aac	acc	tgt	aat	gag	tat	984
Leu	Leu	Lys	Glu	Ala	Ala	Lys	Lys	Met	Ile	Asn	Thr	Cys	Asn	Glu	Tyr	
		275					280					285				

cag	aaa	aga	cac	ggt	aaa	aag	aca	ctc	ttt	gag	gta	cct	gaa	gtc	tga	1032
Gln	Lys	Arg	His	Gly	Lys	Lys	Thr	Leu	Phe	Glu	Val	Pro	Glu	Val		
	290					295				300						

taagcgatta	ttctctccat	gtactcaagg	tataagggtt	atcacatt	1080
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<210> 28  
 <211> 303  
 <212> PRT  
 <213> Escherichia coli

<400> 28

Met	Thr	Glu	Ile	Val	Ala	Asp	Lys	Thr	Val	Glu	Val	Val	Lys	Asn	Ala
1				5					10					15	

Ile	Glu	Thr	Ala	Asp	Gly	Ala	Leu	Asp	Leu	Tyr	Asn	Lys	Tyr	Leu	Asp
			20					25					30		

Gln	Val	Ile	Pro	Trp	Gln	Thr	Phe	Asp	Glu	Thr	Ile	Lys	Glu	Leu	Ser
			35				40					45			

Arg	Phe	Lys	Gln	Glu	Tyr	Ser	Gln	Ala	Ala	Ser	Val	Leu	Val	Gly	Asp
	50					55					60				

Ile	Lys	Thr	Leu	Leu	Met	Asp	Ser	Gln	Asp	Lys	Tyr	Phe	Glu	Ala	Thr
65					70					75				80	

Gln	Thr	Val	Tyr	Glu	Trp	Cys	Gly	Val	Ala	Thr	Gln	Leu	Leu	Ala	Ala
				85					90					95	

Tyr	Ile	Leu	Leu	Phe	Asp	Glu	Tyr	Asn	Glu	Lys	Lys	Ala	Ser	Ala	Gln
		100						105					110		

Lys	Asp	Ile	Leu	Ile	Lys	Val	Leu	Asp	Asp	Gly	Ile	Thr	Lys	Leu	Asn
		115					120					125			

Glu Ala Gln Lys Ser Leu Leu Val Ser Ser Gln Ser Phe Asn Asn Ala  
130 135 140

Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser  
145 150 155 160

Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Lys Ile Arg Lys Glu  
165 170 175

Ala Tyr Ala Gly Ala Ala Ala Gly Val Val Ala Gly Pro Phe Gly Leu  
180 185 190

Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Val Glu Gly Lys Leu Ile  
195 200 205

Pro Glu Leu Lys Asn Lys Leu Lys Ser Val Gln Asn Phe Phe Thr Thr  
210 215 220

Leu Ser Asn Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys  
225 230 235 240

Leu Lys Leu Thr Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu  
245 250 255

Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser  
260 265 270

Leu Leu Lys Glu Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr  
275 280 285

Gln Lys Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Glu Val  
290 295 300